A Comparative Analysis of Data-Augmented DCGAN and SVM-Based Approaches for Malignant Cutaneous Melanoma Neoplasm Identification

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Abstract

Melanoma is one of the deadliest and most prevalent forms of cancer, necessitating the use of advanced tools to aid in its identification, particularly those leveraging artificial intelligence. A novel deep convolutional generative adversarial network (DCGAN) was created to validate the efficacy of its discriminator for the identification of malignant melanoma neoplasms (tumors) in comparison to a traditional support vector machine (SVM). An online dataset was used for both models, however, the limited size required the use of data augmentation to give the illusion of a larger dataset, which included producing new images by various transformations and translations to existing images. Although the SVM performed better, the DCGAN performed well enough to warrant future research into its usage, which could possibly implement a stronger underlying computing framework and a tailored pre-trained architecture to maximize performance.

1 Introduction

Cutaneous melanoma is the deadliest form of cancer affecting the integumentary system, caused by overstimulated ultraviolet radiation to melanocytes, which are skin cells that sit at the basal level of the epidermis and produce melanin (Cichorek et al., 2013; Davis et al., 2019). The resultant malignant neoplasms (tumors) from cutaneous melanoma can lead to skin lesions or discolorations, as well as the growth of moles (Mayo Clinic, 2023).

Although traditional non-invasive melanoma imaging techniques do exist for improving the rate of melanoma neoplasm diagnosis, they typically require an external doctor or skilled practitioner to interpret such images (Patel et al., 2023).

This dependency, therefore, has led to a rise in artificial intelligence (AI)-based solutions that can independently categorize and assess melanoma neoplasms which are typically supervised and use labeled training data for future predictions (Jiang et al., 2020). Common architectures from least to most computationally complex include support vector machines (SVMs), random decision forests, and convolutional neural networks (CNNs) (Mohamed et al., 2022).

A subset of AI, generative AI (GAI), is focused on synthesizing new data and content from the patterns and trends inherent in existing data (Lv, 2023). One primary architecture underlying GAI is the generative adversarial network (GAN), which consists of two neural networks in a zero-sum game. The generator attempts to synthesize new content from random noise, and the discriminator attempts to correctly identify if a presented sample is real or generated. Both neural networks use an algorithm known as *back-propagation* to continuously enhance performance (Aggarwal et al., 2021).

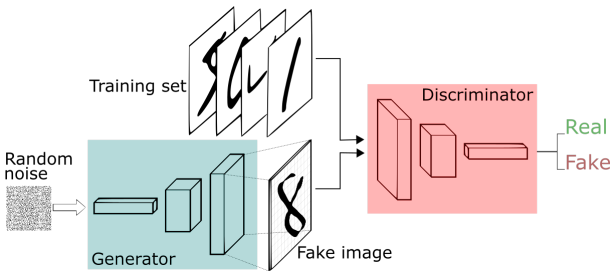

Figure 1: Overview of generative adversarial network (GAN) architecture (Silva, 2017)

Deep Convolutional GANs, or DCGANs, are modified versions of traditional GANs that incorporate aspects of the aforementioned CNNs, namely transposed *convolutional layers* to better capture spatial patterns and hierarchies within data (Radford et al., 2015). There has been little research analyzing the usage of a DCGAN's discriminator for the purpose of malignant melanoma neoplasm identification, compared to a baseline architecture like an SVM, a mathematical model that calculates the optimal *hyperplane* between groups of data (Hearst et al., 1998). The hallmark of GANs are typically their generative capabilities, but this paper focuses on their classification capabilities via their discriminator.

This paper aims to answer the following: *To what extent is a deep convolutional generative adversarial approach effective in malignant melanoma neoplasm identification in comparison with a traditional SVM-based approach?*

2 Methods

In order to train, test, and compare the DCGAN and SVM models, a dataset was used from the online data repository Kaggle, seen *here*. There were a total of 10000 images (5000 benign and 5000 malignant neoplasms) all at a 300

x 300-pixel resolution, with images collected sparsely from International Skin Imaging Collection datasets (Javid, 2022).

This dataset size, although somewhat feasible for the SVM, is nowhere near the volume required for quality results to be produced by the DCGAN, particularly because of the texture and detail required for classifying benign and malignant melanoma neoplasms. Therefore, *data augumentation* was used, which is defined as the process of creating new data from existing data sources (Shorten et al., 2019). The data augmentation consisted of varied shifts and rotations, image shears, scale changes, and flips to the existing images. Each original image was augmented to produce four more images, leading to a total dataset size of 50,000, with 25,000 benign images and 25,000 malignant images. Augmentation was done independently for the DCGAN and SVM, however, the same parameters were used in the `ImageDataGenerator` function from `tensorflow.keras.preprocessing.image`.

The source code of both the DCGAN and SVM models are seen in this *GitHub repository*. Please note that the SVM model used the `sklearn` Python library and its base SVM model. On top of this, various image *feature extraction techniques* were tested, including Gabor filter kernels, Local Binary Patterns (LBP), and Histogram of Oriented Gradients (HOG).

3 Results

The overall results of SVM models are seen below. Note that HOG was chosen for feature extraction on the augmented dataset due to it having the best performance on the non-augmented dataset:

Table 1: SVM accuracies prior to and after data augmentation

Model	Accuracy	Dataset Size
Base SVM	0.810	10000 (5000 benign/malignant)
SVM with LBP	0.822	10000 (5000 benign/malignant)
SVM with Gabor filter kernels	0.827	10000 (5000 benign/malignant)
SVM with HOG	0.831	10000 (5000 benign/malignant)
SVM with HOG	0.879	50000 (25000 benign/malignant)

The DCGAN models showed to be much more responsive to the data augmentation pipeline:

Table 2: DCGAN discriminator accuracies prior to and after data augmentation

Model	Accuracy	Dataset Size
DCGAN discriminator	0.518	10000 (5000 benign/malignant)
DCGAN discriminator	0.791	50000 (25000 benign/malignant)

4 Discussion

The purpose of this research was to analyze the efficacy of a novel DCGAN's discriminator in the identification of malignant melanoma neoplasms.

4.1 Analysis

From the results seen in Tables 1 and 2, it is clear that although the DCGAN did demonstrate far more substantial growth in performance after the implementation of data augmentation, the SVM models performed much more reliably, making it the definitive choice for small-scale data sets. However, the DCGAN's growth implies that a larger dataset could allow the DCGAN to supersede the SVM in performance, with an albeit larger computational barrier-to-entry. The DCGAN's much more nuanced ability to capture detail with its convolutional layers makes it a better choice for more powerful research work.

Furthermore, HOG was found to be the most effective feature extraction technique for malignant melanoma neoplasm identification. For clarity, HOG is a shape-based feature extraction technique that utilizes changes in pixel brightness (known as gradients) and uses them to infer the edges of shapes, which are then intrinsically categorized into groups. (Dalal & Triggs, 2005). This generally aligns with traditional scientific practice, as the shape of supposed melanoma-originating lesions or discolorations is critical for the overall diagnosis (Mayo Clinic, 2023).

4.2 Limitations and Future Research

The limitations found in this research act as the genesis of future research and development into the intersection of artificial intelligence and medical imagery. The lack of a contiguous labeled image dataset for melanoma imagery purposes severely hindered the training and accuracy of both models, particularly the DCGAN, which requires vast throughput data to generate conclusive output. Future research into a non-augmented dataset of collected, standardized images of melanoma neoplasms would greatly aid the use of more complex technologies.

The lack of a strong computing base, particularly a strong GPU, limited the developmental complexity of the novel DCGAN, which could have hindered its possible performance had it been more complex. Implementing a DCGAN with a stronger underlying computational framework in addition to implementing a tailored pre-designed GAN architecture (i.e. StyleGAN or CycleGAN) could boost results for that model.

Although melanoma was the chosen disease for this paper, this comparative imagery concept can be applied to a multitude of other diseases in future research: analyzing mammograms for early breast cancer diagnosis, CT scans for lung cancer, or echocardiograms for the diagnosis of possible cardiovascular diseases.

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